

Table 1: Structural and Function Properties of Transcription-Factor DNA-Binding Domains Chosen for This Study

transcription factor	domain residues ^a	structural class	quaternary state ^b	recognition target (bp) ^c	reported K_d (pM)
Egr-1	332–421	3 zinc-fingers	monomer	10	10–12 ^d 125–170 ^e
GATA-1	158–223	zinc-finger	monomer	6	8300 ^f
GAGA	310–372	zinc-finger	monomer	7	5200 ^g
Cro repressor	1–66	helix–turn–helix	dimer	17	2.0 ^h

^a Numbering of the DNA-binding domain in the native protein. ^b Quaternary state of the protein when bound to DNA. ^c Length of recognition targets in base pairs based on the DNA footprint observed in three-dimensional structures. ^d Range of values from EMSA using Egr-1 ZFD in the *absence* of poly(dI/dC) (28–30). ^e Range of values from EMSA using Egr-1 ZFD in the *presence* of poly(dI/dC) (18, 37). ^f Result from EMSA using isolated GATA-1 ZFD in low ionic-strength buffer (19). ^g Result from EMSA using isolated GAGA factor ZFD in intermediate ionic-strength buffer (38). ^h Result from the filter-binding assay using the full-length Cro repressor (21).